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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention the computation was performed at the SIB using the BLAST network service uses a server developed at SIB and the BLAST 2 software.

In case of problems, please read the online BLAST help.

If your question is not covered, please contact <helpdesk@expasy.org;

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Mille: Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 80 AA

Date run: 2006-04-25 16:35:57 UTC+0100 on blast01.vital-it.ch

Program: NCBI BLASTP 2.2.13 [Nov-27-2005]

Database: UniProtKB

3,037,447 sequences; 998,712,776 total letters

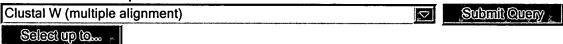
UniProt Knowledgebase Release 7.5 consists of:

UniProtKB/Swiss-Prot Release 49.5 of 18-Apr-2006: 216380 entries UniProtKB/TrEMBL Release 32.5 of 18-Apr-2006: 2807081 entries



List of potentially matching sequences

Send selected sequences to



Include query sequence

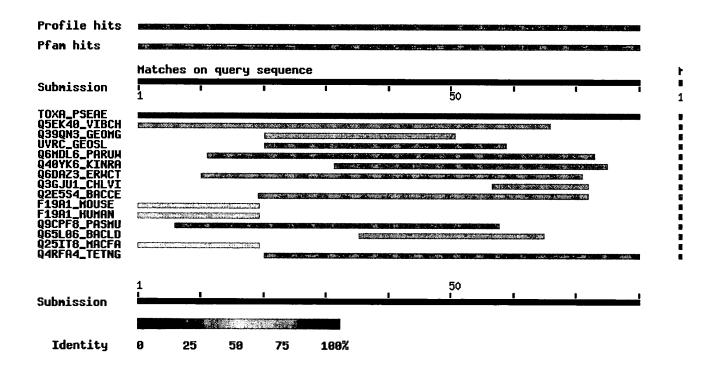
Db AC Description

☑ sp P11439 TOXA_PSEAE Exotoxin A precursor (NAD-dependent ADP-rib.
☑ tr Q5EK40 VIBCH Hypothetical exotoxin A [toxA] [Vibrio cholerae]

Graphical overview of the alignments

to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(Help) (use ScanProsite for more details about PROSITE matches)



Alignments

sp P11439 TOXA PSEAE

Exotoxin A precursor (NAD-dependent ADP-ribosyltransferase) (EC

2.4.2.-) [eta] [Pseudomonas aeruginosa]

Score = 206 bits (469), Expect = 1e-52Identities = 80/80 (100%), Positives = 80/80 (100%)

Query: 1 HRLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAA

HRLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAA

Sbjct: 271 HRLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAA

Query: 61 NQVDQVIRNALASPGSGGDL 80

NQVDQVIRNALASPGSGGDL

Sbjct: 331 NQVDQVIRNALASPGSGGDL 350

tr Q5EK40 Hypothetical exotoxin A [toxA] [Vibrio cholerae]
Q5EK40 VIBCH

Score = 68.1 bits (149), Expect = 5e-11 Identities = 26/66 (39%), Positives = 42/66 (63%)

Query: 1 HRLHFPEGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAA

+R+HF +G +++AL AH+ C +PLET R R+PR C Y Q +V+L++A

Sbjct: 291 QRIHFSKGNAMSALAAHRVCGVPLETLARSRKPRDLTDDLSCAYQAQNIVSLFVAT

Query: 61 NQVDQV 66

++D V

Sbjct: 351 SHLDSV 356

Score = 33.6 bits (69), Expect = 1.1 Identities = 14/31 (45%), Positives = 18/31 (58%)

Query: 21 HLPLETFTRHRQPRGWEQLEQCGYPVQRLVA 51 H PLET R R+P QL QC P + L++ Sbjct: 151 HYPLETCRRRRRPCLFYQLRQCSAPCHGLIS 181

sp Q74717 UvrABC system protein C (Protein uvrC) (Excinuclease ABC 61: UVRC_GEOSL subunit C) AA [uvrC] [Geobacter sulfurreducens]

```
Score = 32.7 bits (67), Expect = 2.1
 Identities = 18/51 (35%), Positives = 24/51 (47%), Gaps = 12/51 (2
Ouerv: 21
           HLPLETFTRHRQPRGWEQLEQCGYPVQRLV-----ALYLAARLS 59
           H PLE+
                   R R+P
                            QL QC P + L+
                                                      AL+LA + S
Sbjct: 151 HYPLESCRRRRPCLFYQLRQCAAPCHGLISGEDYQSLAEGAALFLAGKNS 201
tr
    Q6MDL6
                       Hypothetical protein [pc0609] [Parachlamydia sp.
    Q6MDL6 PARUW
                        subsp.
                       Acanthamoeba sp. (strain UWE25)]
 Score = 32.3 bits (66), Expect = 2.8
 Identities = 19/62 (30%), Positives = 30/62 (48%), Gaps = 12/62 (1
Query: 12 AALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQVI
           A+++AH+
                                            ΥP
                                               +L+AL
                    + LE
                            + R
Sbjct: 91 ASVSAHEGAYYILEAGLKNR------YPQIQLIALNTLARLQSDKADQTI
Query: 72 AS 73
            S
Sbjct: 139 GS 140
tr Q40YK6
              Phosphoesterase PHP, N-terminal: PHP, C-terminal
                                                                 381
   Q40YK6 KINRA [KradDRAFT 1289]
                                                                 AA
              [Kineococcus radiotolerans SRS30216]
                                                                 aligr
 Score = 32.3 \text{ bits (66)}, Expect = 2.8
 Identities = 17/46 (36%), Positives = 24/46 (52%), Gaps = 2/46 (4%)
Query: 32 QPRGWEQLEQCGYPVQRLVALYLAAR-LSWN-QVDQVIRNALASPG 75
           QPG + ++CGP+R+V + ARLWQ
                                                  RA+PG
Sbjct: 336 QPYGCARAQECGVPAERIVTTWPAERVLEWTAQRRSAHRPARPAPG 381
tr
    Q6DAZ3
                       Hypothetical protein [ECA0109] [Erwinia carotovora
    Q6DAZ3 ERWCT
                       subsp.
                       atroseptica (Pectobacterium atrosepticum)]
 Score = 31.9 \text{ bits } (65), Expect = 3.8
 Identities = 22/61 (36%), Positives = 28/61 (45%), Gaps = 14/61 (2
Query: 11 LAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQV
           +AA+ HQA HL LE H + R
                                              P + RL + + Y R
                                                               NOV
```

Sbjct: 259 MAAVVPHQASHLSLE----HMRKR-----LAIPTERLIDIY---RYHGNOVAAS Query: 71 L 71 Sbjct: 305 L 305 Transposase, IS204/IS1001/IS1096/IS1165 [CvibDRAFT 1521] 406 AA tr 03GJU1 Q3GJU1_CHLVI [Prosthecochloris vibrioformis DSM 265] align Score = 31.9 bits (65), Expect = 3.8Identities = 11/16 (68%), Positives = 13/16 (81%) Query: 57 RLSWNQVDQVIRNALA 72 RLSW VDQ++R ALA Sbjct: 129 RLSWHSVDQIMRRALA 144 tr Q2E5S4 Hypothetical protein [Bcer98DRAFT 0450] [Bacillus cereus 172 Q2E5S4 BACCE subsp. AΑ cytotoxis NVH 391-98] aligr Score = 31.4 bits (64), Expect = 5.1Identities = 19/53 (35%), Positives = 28/53 (52%), Gaps = 2/53 (3%) Query: 20 CHLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQVIRNALA 72 LE + + + PRG +Q V+LY RL WN G ++I+A+ASbjct: 22 CHEVLEEYWKLK-PRGKRDHHWVGL-IQIAVSLYHQRRLNWNGAAKMIKRAIA 72 sp Q7TPG8 Protein FAM19A1 precursor (Chemokine-like protein TAFA-1) 133 AA F19A1 MOUSE [Fam19a1] [Mus musculus (Mouse)] align Score = 31.0 bits (63), Expect = 6.8Identities = 10/20 (50%), Positives = 13/20 (65%) Query: 1 HRLHFPEGGSLAALTAHQAC 20 H LH PEGG+ + AH+ C Sbjct: 34 HHLHRPEGGTCEVIAAHRCC 53

sp Q7Z5A9 Protein FAM19A1 precursor (Chemokine-like protein TAFA-1) 133 AA

```
F19A1 HUMAN [FAM19A1] [Homo sapiens (Human)]
                                                                     align
 Score = 31.0 \text{ bits } (63), \text{ Expect} = 6.8
 Identities = 10/20 (50%), Positives = 13/20 (65%)
Query: 1 HRLHFPEGGSLAALTAHQAC 20
           H LH PEGG+
                         + AH+ C
Sbjct: 34 HHLHRPEGGTCEVIAAHRCC 53
tr
     Q9CPF8
                           HofB [hofB] [Pasteurella multocida]
                                                                    461 AA
     Q9CPF8_PASMU
                                                                    align
 Score = 31.0 \text{ bits } (63), Expect = 6.8
 Identities = 19/55 (34%), Positives = 27/55 (49%), Gaps = 3/55 (5%)
Query: 7
            EGGSLAALTAHQACHLPLETFTRHRQPRGWEQLEQCGYP---VORLVALYLAARL
               +L AL A Q HL L T
                                         Ρ
                                              +L+Q G P
                                                          +++ + L +A RL
Sbjct: 337 EESALIALRAAQTGHLVLSTLHTNDAPSALTRLQQLGVPLHEIEQSLLLVVAQRL
tr Q65L06
               Hypothetical DNA-binding protein, putative
                                                                      225
   Q65L06 BACLD transcriptional regulator
                                                                     AA
               [BL03804] [Bacillus licheniformis (strain DSM 13 / ATCC
                                                                     align
               14580)]
 Score = 31.0 \text{ bits } (63), Expect = 6.8
 Identities = 12/30 (40%), Positives = 16/30 (53%)
Query: 36 WEQLEQCGYPVQRLVALYLAARLSWNQVDQ 65
              ++0
                      P QR+ L LAA
                                       WN + Q
Sbjct: 151 WAAIQQMNVPFQRIRFLRLAADFNWNTIHQ 180
tr Q25IT8
               Brain cDNA, clone: QflA-18513 [Macaca fascicularis (Crab 133
   Q25IT8 MACFA eating
                                                                     AΑ
               macaque) (Cynomolgus monkey)]
                                                                     align
 Score = 31.0 \text{ bits } (63), \text{ Expect} = 6.8
 Identities = 10/20 (50%), Positives = 13/20 (65%)
Ouerv: 1 HRLHFPEGGSLAALTAHOAC 20
           H LH PEGG+
                         + AH+ C
```

Sbjct: 34 HHLHRPEGGTCEVIAAHRCC 53

```
tr
     Q4RFA4
                        Chromosome 8 SCAF15119, whole genome shotgun
     Q4RFA4 TETNG
                        sequence
                        [GSTENG00035413001] [Tetraodon nigroviridis (Green
                        puffer) ]
  Score = 30.6 bits (62), Expect = 9.2
  Identities = 21/71 (29%), Positives = 33/71 (46%), Gaps = 11/71 (1
 Query: 21 HLPLETFTRHRQPRGWEQLEQCGYPVQRLVALYLAARLSWNQVDQ-------
                         R E+L+ G
                    +H+
                                     +
                                            + +A+R S N VD
 Sbjct: 245 HIPKTATAKHKGRREGEELDSQGDASSQPDTISIASRTSQNTVDSDKLSGGCELTV
 Ouerv: 70
           ALASPGSGGDL 80
             +AS GS G+L
 Sbjct: 305 FVASNGSSGEL 315
Database: UniProtKB
    Posted date: Apr 17, 2006 4:33 PM
  Number of letters in database: 996,967,394
  Number of sequences in database: 3,032,459
  Database: /home/local/blastnet/database/EXPASY//UniProtKB.01
    Posted date: Apr 17, 2006 4:34 PM
  Number of letters in database: 1,745,382
  Number of sequences in database: 4988
Lambda
           K
                  Η
          0.176
  0.340
                    0.689
Gapped
Lambda
           K
  0.299 0.0710
                    0.270
Matrix: BLOSUM80
Gap Penalties: Existence: 10, Extension: 1
Number of Hits to DB: 129,822,965
Number of Sequences: 3037447
Number of extensions: 2444038
Number of successful extensions: 13677
Number of sequences better than 10.0: 15
Number of HSP's better than 10.0 without gapping: 9
Number of HSP's successfully gapped in prelim test: 6
Number of HSP's that attempted gapping in prelim test: 13668
Number of HSP's gapped (non-prelim): 15
length of query: 80
```

```
length of database: 998,712,776
effective HSP length: 62
effective length of query: 18
effective length of database: 810,391,062
effective search space: 14587039116
effective search space used: 14587039116
T: 12
A: 25
X1: 15 ( 7.4 bits)
X2: 34 (14.7 bits)
X3: 57 (24.6 bits)
S1: 39 (21.7 bits)
S2: 62 (30.6 bits)
Wallclock time: 3 seconds
```

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L4: Entry 2 of 118

File: USPT

Apr 18, 2006

DOCUMENT-IDENTIFIER: US 7030215 B2

TITLE: Position dependent recognition of GNN nucleotide triplets by zinc fingers

PRIOR-PUBLICATION:

DOC-ID

DATE

US 20030068675 A1

April 10, 2003

Description Paragraph (49):

Toxin molecules also have the ability to transport polypeptides across cell membranes. Often, such molecules are composed of at least two parts (called "binary toxins"): a translocation or binding domain or polypeptide and a separate toxin domain or polypeptide. Typically, the translocation domain or polypeptide binds to a cellular receptor, and then the toxin is transported into the cell. Several bacterial toxins, including Clostridium perfringens iota toxin, diphtheria toxin (DT), Pseudomonas exotoxin A (PE), pertussis toxin (PT), Bacillus anthracis toxin, and pertussis adenylate cyclase (CYA), have been used in attempts to deliver peptides to the cell cytosol as internal or amino-terminal fusions (Arora et al., J. Biol. Chem., 268:3334 3341 (1993); Perelle et al., Infect. Immun., 61:5147 5156 (1993); Stenmark et al., J. Cell Biol. 113:1025 1032 (1991); Donnelly et al., PNAS 90:3530 3534 (1993); Carbonetti et al., Abstr. Annu. Meet. Am. Soc. Microbiol. 95:295 (1995); Sebo et al., Infect. Immun. 63:3851 3857 (1995); Klimpel et al., PNAS U.S.A. 89:10277 10281 (1992); and Novak et al., J. Biol. Chem. 267:17186 17193 1992)).

Previous Doc Next Doc Go to Doc#

First Hit Fwd Refs

Previous Doc Next Doc Go to Doc#

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L2: Entry 9 of 14

File: USPT

Oct 16, 2001

DOCUMENT-IDENTIFIER: US 6303120 B1

** See image for Certificate of Correction **

TITLE: Synthesis of glycoconjugates of the lewis y epitope and uses thereof

CLAIMS:

4. The method of claim 1, wherein the antibodies bind to $\underline{\text{Lewis Y expressing}}$ epithelial tumor cells.

Previous Doc Next Doc Go to Doc#

INTERNATIONAL SEARCH REPORT

Int stonet Application No PCT/US 98/14341

A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/62 A61K A61K39/21 C07K16/10 A61K39/104 C12N15/70 A61K48/00 According to International Patent Classification (IPC) or to both national classification and IPC Minimum documentation searched (classification system followed by classification symbols) C12N A61K C07K IPC 6 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practical, search terms used) C. DOCUMENTS CONSIDERED TO BE RELEVANT Citation of document, with indication, where appropriate, of the relevant passages Category ⁴ Relevant to claim No. EP 0 439 954 A (SERAGEN, INC.) 1-5,7,8, 7 August 1991 12, 15-20, 22-24, 26-43 see page 2, line 45 - page 3, line 50 see page 4, line 1 - 1 ine 40see page 5, line 23 - line 53 see page 11, line 35 - page 12, line 26 -/--Further documents are listed in the continuation of box C. Patent family members are listed in annex. X | Special categories of cited documents : "T" later document published after the international filing date or priority date and not in conflict with the application "A" document defining the general state of the art which is not considered to be of particular relevance cited to understand the principle or theory underlying the invention "E" earlier document but published on or after the international "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "O" document referring to an oral disclosure, use, exhibition or other means document published prior to the international filing date but later than the priority date claimed "&" document member of the same patent family Date of the actual completion of theinternational search Date of mailing of the international search report 27 October 1998 10/11/1998 Name and mailing address of the ISA Authorized officer European Patent Office, P.B. 5818 Patentiaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Montero Lopez, B Fax: (+31-70) 340-3016

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INTERNATIONAL SEARCH REPORT

In. utional Application No PCT/US 98/14341

		FC1/US 96/14341	
C.(Continue Category *	etion) DOCUMENTS CONSIDERED TO BE RELEVANT Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	
Calegory	Chapter of document, with independent relationship to the relation passages	Markata to dalli No.	
Y	VIJAY . CHAUDHARY ET AL.: "Pseudomonas exotoxin contains a specific sequence at the carboxyl terminus that is required for cytotoxicity" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 87, no. 1, January 1990, pages 308-312, XP002079997 WASHINGTON US see abstract see page 308, right-hand column, paragraph 2	1,3-5,7, 8,15-20, 22-24, 26-43	
Υ	MAJA LUKAC ET AL.: "Toxoid of Pseudomonas aeruginosa Exotoxin A generated by deletion of an ctive site residue" INFECTION AND IMMUNITY., vol. 56, no. 11, November 1988, pages 3095-3098, XP002080494 WASHINGTON US see abstract	2,12	
A	S.J. CRYZ JR ET AL.: "Human immunodeficiency virus—1 principal neutralizing domain peptide—toxin A cnjugate vaccine" VACCINE., vol. 13, no. 1, January 1995, pages 67-71, XP002079998 GUILDFORD GB cited in the application see abstract see page 67, left—hand column, paragraph 1—right—hand column, paragraph 1 see page 69, left—hand column, paragraph 2 see page 70, right—hand column, paragraph 1—page 71, left—hand column, paragraph 1—right—hand column, paragraph 1—r		
Ρ,Χ	DAVID J. FITZGERALD ET AL.: "Characterization of V3 loop-Pseudomonas Exotoxin chimeras" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 16, 17 April 1998, pages 9951-9958, XP002079999 MD US see the whole document	1-43	
T	WO 98 20135 A (THE GOVERNMENT OF THE UNITED STATES OF AMERICA) 14 May 1998 see page 4, line 4 - line 32 see page 22, line 40 - line 50 see page 23, line 22 - page 25, line 2 see page 27, line 18 - page 29, line 5 see page 31, line 2 - page 32, line 12		

1

remational application No.

INTERNATIONAL SEARCH REPORT

PCT/US 98/14341

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. X Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely: Remark: Although claims 24-26, 33-38, and 40-43 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows:
As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

information on patent family members

Int tional Application No PCT/US 98/14341

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
EP 439954	A	07-08-1991	AU	657087 B	02-03-1995
			AU	7168991 A	24-07-1991
			AU	8032194 A	27-04-1995
			CA	2071969 A	23-06-1991
			JP	5502880 T	20-05-1993
			WO	9109871 A	11-07-1991
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